

Figure 1. Amino acid sequence alignment in human IgG isotypes and their variants.

Human IgG Isotype	Amino Acid Position				
	228.....234	235	236	237.....330	331
G1	Pro.....Leu	Leu	Gly	Gly.....Ala	Pro
G2	Pro.....Val	Ala	Gly.....Ala	Pro
G4	Ser.....Phe	Leu	Gly	Gly.....Ser	Ser
G1 variant	Pro..... Val	Ala	Gly	Gly.....Ala	Ser
G2 variant	Pro.....Val	Ala	Gly.....Ala	Ser
G4 variant	ProPhe	Ala	Gly	Gly.....Ser	Ser

tgc cca ccg tgc cca gca cca cct gtg gca gga ccg tca gtc ttc ctc ttc ccc cca aaa 720
 C P P C P A P P P V A G P S V F L F P P K
 190
 ccc aag gac acc ctc atg atc tcc cgg acc cct gag gtc acg tgc gtg gtg gac gtg 780
 P K D T L M I S R T P E V T C V V D V
 210
 agc cac gaa gac ccc gag gtc cag ttc aac tgg tac gtg gac ggc gtg gag gtg cat aat 840
 S H E D P E V Q F N W Y V D G V E V H N
 230
 gcc aag aca aag cca cgg gag gag ttc aac agc agc ttc cgt gtg gtc agc gtc ctc 900
 A K T K P R E E Q F N S T F R V V S V L
 250
 acc gtt gtg cac cag gac tgg ctg aac ggc aag gac tac aag tgc aag gtc tcc aac aaa 960
 T V V H Q D W L N G K E Y K C K V S N K
 270
 ggc ctc cca gcc tcc atc gag aaa acc atc tcc aaa acc aaa ggg cag ccc cga gaa cca 1020
 G L P A I E K T I S K T K K G Q P R E P
 290
 cag gtg tac acc ctg ccc cca tcc cgg gag gag atg acc aag aac cag gtc agc ctg acc 1080
 Q V Y T L P P S S R E E M T K N Q V S L T
 310
 tgc ctg gtc aaa ggc ttc tac ccc agc gac atc gcc gtg gag tgg gag agc aat ggg cag 1140
 C L V K G F Y Y P P S D I A V E W E S N G Q
 330
 ccg gag aac aac tac aag acc aca cct ccc atg ctg gag tcc gac ggc tcc ttc ttc ctc 1200
 P E N N Y K T T P P M L S D G S F F L
 350
 tac agc aag ctc acc ctg gac aag agc agg tgg cag ggg aac gtc ttc tca tgc tcc 1260
 Y S K L T V D K S R W Q Q G N V F S C S
 370
 gtg atg cat gag gct ctg cac aac cac tac acg cag aag agc ctc tcc ctg tct ccg ggt 1320
 V M H E A L H N H Y T Q K S L S P G
 390
 aaa tga gaa ttc 1332
 K EcoRI
 409

25

25

[illegible]

27

27

ccg tgc cca gca cct gaa gtc gcg ggg gga ccg tca gtc ttc ctg ttc ccc cca aaa ccc
 P C P A P E V A 720
 190
 aag gac acc ctg atc tcc cgg aca cct gag gtc aca tgc gtg gtg gac gtg agc
 K D T L M I S R T P E V 200
 210
 cac gaa gac cct gag gtc aag ttc aac tgg tac gtg gac ggc gtg gag gtg cat aat gcc
 H E D P E V K F N W Y 220
 230
 aag aca aag ccg cgg gag gag cag tac aac agc acg tac cgg gtg gtc agc gtc ctc acc
 K T K P R E E Q Y N S T Y R V S V L T 900
 250
 gtc ctg cac cag gac tgg ctg aat ggc aag gag tac aag tgc aag gtc tcc aac aaa gcc
 V L H Q D W L N G K E Y K C K V S N K A 960
 270
 ctg cca gcc tcc atc gag aaa acc atc tcc aa ggc cag ccg cca gaa cca cag
 L P A s I E K T I S K A 1020
 290
 gtg tac acc ctg ccc cca tcc cgg gat gag ctg acc gag aac cag gtc agc ctg acc tgc
 V Y T L P P S R D E L T K N Q V S L T C 1080
 310
 ctg gtc aaa ggc ttc tat ccc agc gac atc gcc gtg gag tgg gag agc aat ggg cag ccg
 L V K G F Y P S D I A V E W E S N G Q P 1140
 330
 gag aac aac tac aag acc acg cct ccc gtg ctg gac tcc gac ggc tcc ttc ttc ctc tac
 E N N Y K T T P P V L D S S D G S F L Y 1200
 350
 agc aag ctg acc ctg gac aag agc agg tgg cag cag ggg aac gtc ttc tca tgc tcc gtg
 S K L T V D K S R W Q 360
 370
 atg cat gag gct ctg cac aac cac tac acg cag aag agc ctg tcc ctg tct ccg ggt aaa
 M H E A L H N H Y T Q K S L S L S P G K 1320
 390
 tga gaa ttc
 EcoRI 1329